

## Figure 1

bcl Consensus PCR Primers

Ile

EcoRI AspTrpGlyArgValValAla

5- AGATCTGAATTCAACTTGGGGGIC(A)GIA(G)TXGTXGC -3' bclx 1-32

AspTrpGlyGlyGlnGluAsnAspGlnIleTrp

AGGGTIGGIGGXACXAGA(G)ACA(T)(C)TAGGT

5'- AGATCT'AAGCTTGTCCCAICCCICCTGXTCC(T)TGA(G)ATCCA -3' bclX 2-39

Figure 2

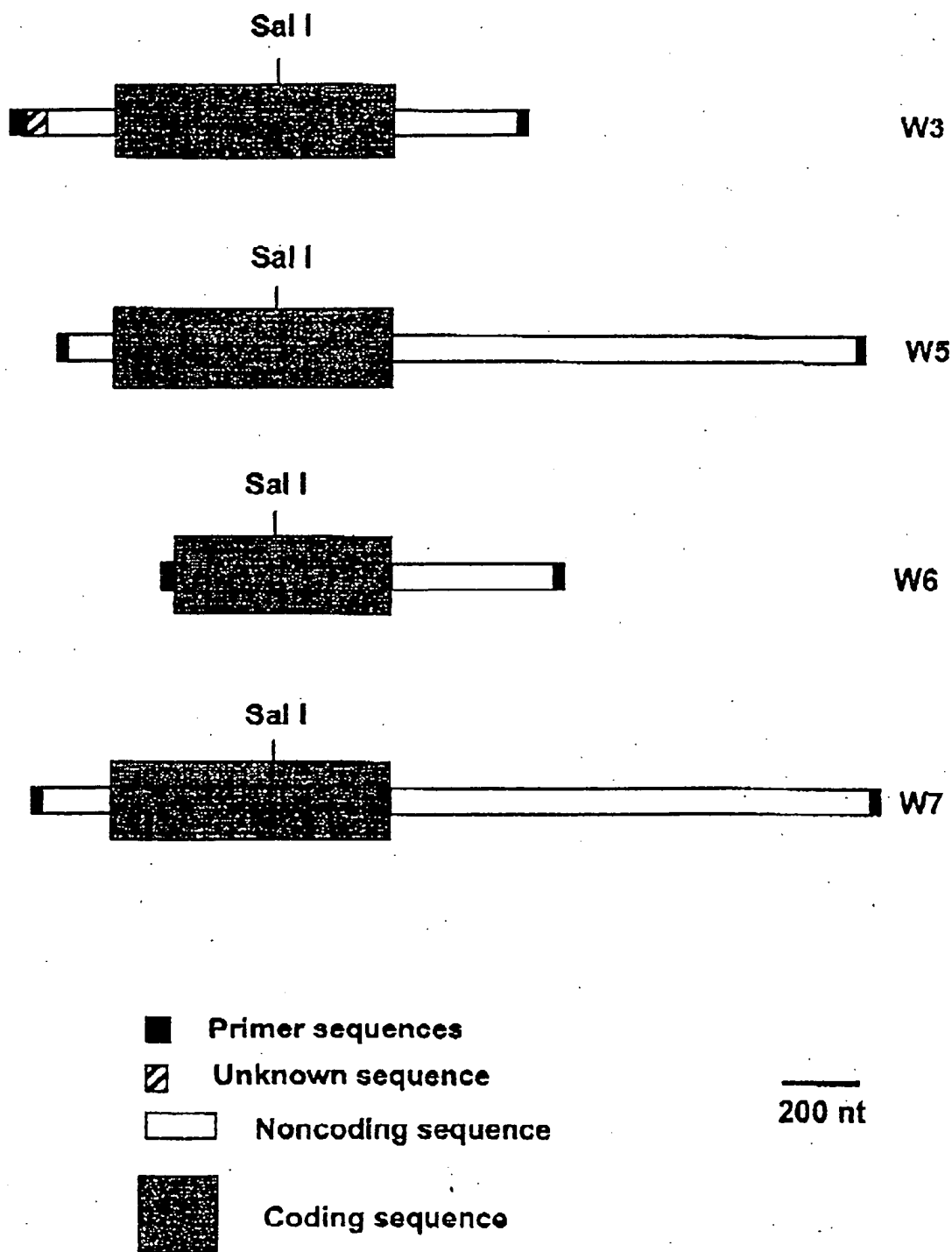
**Cdi-1 cDNA clones**

Figure 3

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      10      20      30      40
      *      *      *      *
GAG GAT CTA CAG GGG ACA AGT AAA GGC TAC ATC CAG ATG CCG GGA ATG
CTC CTA GAT GTC CCC TGT TCA TTT CCG ATG TAG GTC TAC GGC CCT TAC

>Aha2
50      60      70      80      90
*      *      *      *      *
CAC TGA CGC CCA TTC CTG GAA ACT GGG CTC CCA CTC AGC CCC TGG GAG
GTG ACT GCG GGT AAG GAC CTT TGA CCC GAG GGT GAG TCG GGG ACC CTC

100      110      120      130      140
*      *      *      *      *
CAG CAG CCG CCA GCC CCT CGG ACC TCC ATC TCC ACC CTG CTG AGC CAC
GTC GTC GGC GGT CGG GGA GCC TGG AGG TAG AGG TGG GAC GAC TCG GTG

>SmaI      >BamHI
150      160      170      180      190
*      *      *      *      *
CCG GGT TGG GCC AGG ATC CCG GCA GGC TGA TCC CGT CCT CCA CTG AGA
GGC CCA ACC CGG TCC TAG GGC CCT CCG ACT AGG GCA GGA GGT GAC TCT

200      210      220      230      240
*      *      *      *      *
CCT GAA AA ATG GCT TCG GGG CAA GGC CCA GGT CCT CCC AGG CAG GAG TGC
GGA CTT TT TAC CGA AGC CCC GTT CCG GGT CCA GGA GGG TCC GTC CTC ACG
      M  A  S  G  Q  G  P  G  P  P  R  Q  E  C>

250      260      270      280      290
*      *      *      *      *
GGA GAG CCT GCC CTG CCC TCT GCT TCT GAG GAG CAG GTA GCC CAG GAC
CCT CTC CGA CGG GAC GGG AGA CGA AGA CTC CTC GTC CAT CCG GTC CTG
G  E  P  A  L  P  S  A  S  E  E  Q  V  A  Q  D>

300      310      320      330
*      *      *      *
ACA GAG GAG GTT TTC CGC AGC TAC GTT TTT TAC CGC CAT CAG CAG GAA
TGT CTC CTC CAA AAG GCG TCG ATG CAA AAA ATG GCG GTA GTC GTC CTT
T  E  E  V  F  R  S  Y  V  F  Y  R  H  Q  Q  E>

340      350      360      370      380
*      *      *      *      *
CAG GAG GCT GAA GGG GTG GCT GCC CCT GCC GAC CCA GAG ATG GTC ACC
GTC CTC CGA CTT CCC CAC CGA CGG GGA CGG CTG GGT CTC TAC CAG TGG
Q  E  A  E  G  V  A  A  P  A  D  P  E  M  V  T>

>NcoI
390      400      410      420      430
*      *      *      *      *
TTA CCT CTG CAA CCT AGC AGC ACC ATG GGG CAG GTG GGA CCG CAG CTC
AAT GGA GAC GTT GGA TCG TCG TGG TAC CCC GTC CAC CCT GCC GTC GAG
L  P  L  Q  P  S  S  T  M  G  Q  V  G  R  Q  L>

440      450      460      470      480
*      *      *      *      *
GCC ATC ATC GGG GAC GAC ATC AAC CGA CGC TAT GAC TCA GAG TTC CAG
CGG TAG TAG CCC CTG CTG TAG TTG SCT GCG ATA CTG AGT CTC AAG GTC

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Figure 3 cont.

A I I G D D I N R R Y D S E F Q>

>Pst1

490 500 510 520 530

\* \* \* \* \*

ACC ATG TTG CAG CAC CTG CAG CCC ACG GCA GAG AAT GCC TAT GAG TAC  
 TGG TAC AAC GTC GTG GAC GTC GGG TGC CGT CTC TTA CCG ATA CTC ATG  
 T M L Q H L Q P T A E N A Y E Y>

540 550 560 570

\* \* \* \*

TTC ACC AAG ATT GCC ACC AGC CTG TTT GAG AGT GGC ATC AAT TGG GGC  
 AAG TGG TTC TAA CCG TGG TCG GAC AAA CTC TCA CCG TAG TTA ACC CCG  
 F T K I A T S L F E S G I N W G>

580 590 600 610 620

\* \* \* \* \*

CGT GTG GTG GGT CTT CTG GGC TTC GGC TAC CGT CTG GCC CTA CAC GTC  
 GCA CAC CAC CGA GAA GAC CCG AAG CCG ATG GCA GAC CCG GAT GTG CAG  
 R V V A L L G F G Y R L A L H V>

630 640 650 660 670

\* \* \* \* \*

TAC CAG CAT GGC CTG ACT GGC TTC CTA GGC CAG GTG ACC CGC TTC GTG  
 ATG GTC GTA CCG GAC TGA CCG AAG GAT CCG GTC CAC TGG GCG AAG CAC  
 Y Q H G L T G F L G Q V T R F V>

>Seq11

680 690 700 710 720

\* \* \* \* \*

GTC GAC TTC ATG CTG CAT CAC TGC ATT GCC CGG TGG ATT GCA CAG AGG  
 CAG CTG AAG TAC GAC GTA GTG ACG TAA CCG GCC ACC TAA CGT GTC TCC  
 V D F M L H H C I A R W I A Q R>

730 740 750 760 770

\* \* \* \* \*

GGT GGC TGG GTG GCA GCC CTG AAC TTG GGC AAT GGT CCC ATC CTG AAC  
 CCA CCG ACC CAC CGT CCG GAC TTG AAC CCG TTA CCA GGG TAG GAC TTG  
 G G W V A A L N L G N G P I L N>

780 790 800 810

\* \* \* \*

GTG CTG GTG GTT CTG GGT GTG GTT CTG TTG GGC CAG TTT GTG GTA CGA  
 CAC GAC CAC CAA GAC CCA CAC CAA GAC AAC CCG GTC AAA CAC CAT GCT  
 V L V V L G V V L L G Q F V V R>

820 830 840 850 860

\* \* \* \* \*

AGA TTC TTC AAA TCA TGA C TCC CAA GGC TGC CCT TTG GGT CCC GGT TCA  
 TCT AAG AAG TTT AGT ACT G AGG GTT CCC ACG GGA AAC CCA GGG CCA AGT  
 R F F K S \*>

>Af12

870 880 890 900 910

\* \* \* \* \*

GAC CCC TGC CTG GAC TTA AGC GAA GTC TTT GGC TTC TCT GTT CCC TTG  
 CTG GGG ACG GAC CTG AAT TCG CTT CAG AAA CCG AAG AGA CAA GGG AAC

&gt;Hind3

Figure 3 cont.

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      920          930          940          950          960
      *          *          *          *          *
CAG GGT CCC CCC TCA AGA GTA CAG AAG CTT TAG CAA GTG TGC ACT CCA
GTC CCA GGG GGG AGT TCT CAT GTC TTC GAA ATC GTT CAC ACG TGA GGT

                                     >Pst1
                                     |
      970          980          990          1000          1010
      *          *          *          *          *
GCT TCG GAG GCC CTG CGT GGG GGC CAG TCA GGC TGC AGA GGC ACC TCA
CGA AGC CTC CGG GAC GCA CCC CCG GTC AGT CCG ACG TCT CCG TGG AGT

                                     >Apa1
                                     |
      1020          1030          1040          1050
      *          *          *          *
ACA TTG CAT GGT GCT AGT GCC CTC TCT CTG GGC CCA GGG CTG TGG CCG
TGT AAC GTA CCA CGA TCA CGG GAG AGA GAC CCG GGT CCC GAC ACC GGC

1060          1070          1080          1090          1100
      *          *          *          *          *
TCT CCT CCC TCA GCT CTC TGG GAC CTC CTT AGC CCT GTC TGC TAG GCG
AGA GGA GGG AGT CGA GAG ACC CTG GAG GAA TCG GGA CAG ACG ATC CGC

1110          1120          1130          1140          1150
      *          *          *          *          *
CTG GGG AGA CTG ATA ACT TGG GGA GGC AAG AGA CTG GGA GCC ACT TCT
GAC CCC TCT GAC TAT TGA ACC CCT CCG TTC TCT GAC CCT CCG TGA AGA

      1160          1170          1180          1190          1200
      *          *          *          *          *
CCC CAG AAA GTG TTT AAC GGT TTT AGC TTT TTA TAA TAC CCT TGT GAG
GGG GTC TTT CAC AAA TTG CCA AAA TCG AAA AAT ATT ATG GGA ACA CTC

                                     >Aha2
                                     |
      1210          1220          1230          1240          1250
      *          *          *          *          *
AGC CCA TTC CCA CCA TTC TAC CTG AGG CCA GGA CGT CTG GGG TGT GGG
TCG GGT AAG GGT GGT AAG ATG GAC TCC GGT CCT GCA GAC CCC ACA CCC

      1260          1270          1280          1290
      *          *          *          *
GAT TGG TGG GTC TAT GTT CCC CAG GAT TCA GCT AAT CTG GAA CAT CAG
CTA ACC ACC CAG ATA CAA GGG GTC CTA AGT CGA TAA GAC CTT CTA GTC

1300          1310          1320          1330          1340
      *          *          *          *          *
CAC CCT AAG AGA TGG GAC TAG GAC CTG AGC CTG GTC CTG GCC GTC CCT
GTG GGA TTC TCT ACC CTG ATC CTG GAC TCG GAC CAG GAC CCG CAG GGA

1350          1360          1370          1380          1390
      *          *          *          *          *
AAG CAT GTG TCC CAG GAG CAG GAC CTA CTA GGA GAG GGG GGC CAA GGT
TTC GTA CAC AGG GTC CTC GTC CTG GAT GAT CCT CTC CCC CCG GTT CCA

      1400          1410          1420          1430          1440
      *          *          *          *          *
CCT GCT CAA CTC TAC CCC TGC TCC CAT TCC TCC CTC CCG CCA TAC TGC
GGA CGA GTT GAG ATG GGG ACG AGG GTA AAG AGG GAG GCC GGT ATG ACG

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## Figure 3 cont.

1450 * CTT TGC AGT TGG ACT CTC AGG GAT TCT GGG CTT GGG GTG TGG GGT GGG GAA ACG TCA ACC TGA GAG TCC CTA AGA CCC GAA CCC CAC ACC CCA CCC	1460 * 1500 * GTG GAG TCG CAG ACC AGA GCT GTC TGA ACT CAC GTG TCA GAA GCC TCC CAC CTC AGC GTC TGG TCT CGA CAG ACT TGA GTG CAC AGT CTT CGG AGG	1470 * 1510 * 1520 * 1530 *	1480 * 1540 * 1550 * 1560 * 1570 * 1580 *	1490 * 1590 * 1600 * 1610 * 1620 * 1630 *
AAG CCT GCC TCC CAA GGT CCT CTC AGT TCT CTC CCT TCC TCT CTC CTT TTC GGA CGG AGG GTT CCA GGA GAG TCA AGA GAG GGA AGG AGA GAG GAA	ATA GAC ACT TGC TCC CAA CCC ATT CAC TAC AGG TGA AGG CTC TCA CCC TAT CTG TGA ACG AGG GTT GGG TAA GTG ATG TCC ACT TCC GAG AGT GGG	1640 * 1650 * 1660 * 1670 * 1680 *	1690 * 1700 * 1710 * 1720 * 1730 *	1740 * 1750 * 1760 * 1770 *
ATC CCT GGG GGC CTT GGG TGA GTG GCC TGC TAA GGC TCC TCC TTG CCC TAG GGA CCC CCG GAA CCC ACT CAC CGG ACG ATT CCG AGG AGG AAC GGG	AGA CTA CAG GGC TTA GGA CTT GGT TTG TTA TAT CAG GGA AAA GGA GTA TCT GAT GTC CCG AAT CCT GAA CCA AAC AAT ATA GTC CCT TTT CCT CAT	GGG AGT TCA TCT GGA GGG TTC TAA GTG GGA GAA GGA CTA TCA ACA CCA CCC TCA AGT AGA CCT CCC AAG ATT CAC CCT CTT CCT GAT AGT TGT GGT		

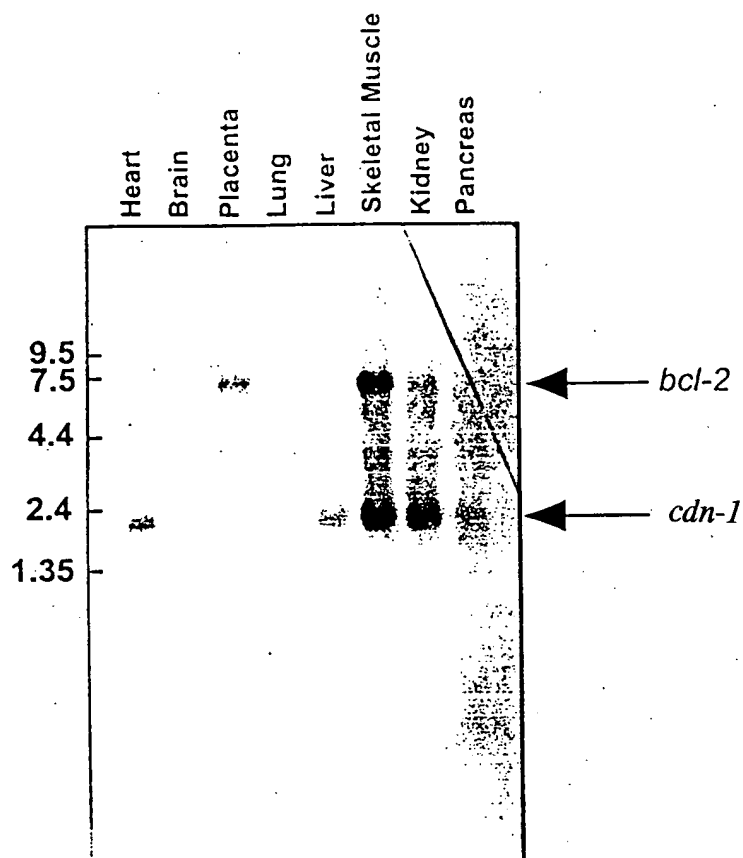
>BamH1

1780 * CTA GGA ATC CCA GAG GTG GAT CCT CCC TCA TGG CTC TGG CAC AGT GTA GAT CCT TAG GGT CTC CAC CTA GGA GGG AGT ACC GAG ACC GTG TCA CAT	1790 * 1800 * 1810 * 1820 *	1830 * 1840 * 1850 * 1860 * 1870 *	1880 * 1890 * 1900 * 1910 * 1920 *	1930 * 1940 * 1950 * 1960 * 1970 *
ATC CAG GGG TGT AGA TGG GGG AAC TGT GAA TAC TTG AAC TCT GTT CCC TAG GTC CCC ACA TCT ACC CCC TTG ACA CTT ATG AAC TTG AGA CAA GGG	CCA CCC TCC ATG CTC CTC ACC TGT CTA GGT CTC CTC AGG GTG GGG GGT GGT GGG AGG TAC GAG GAG TGG ACA GAT CCA GAG GAG TCC CAC CCC CCA	GAC AGT GCC TTC TCT ATT GGC ACA GCC TAG GGT CTT GGG GGT CAG GGG CTG TCA CGG AAG AGA TAA CCG TGT CGG ATC CCA GAA CCC CCA GTC CCC	1980 * 1990 * 2000 * 2010 *	
GGA GAA GTT CTT GAT TCA GCC AAA TGC AGG GAG GGG AGG CAG ATG GAG CCT CTT CAA GAA CTA AGT CGG TTT ACG TCC CTC CCC TCC GTC TAC CTC				

## Figure 3 cont.

2020	2030	2040	2050	2060											
*	*	*	*	*											
CCC	ATA	GGC	CAC	CCC	CTA	TCC	TCT	GAG	TGT	TTG	GAA	ATA	AAC	TGT	GCA
GGG	TAT	CCG	GTG	GGG	GAT	AGG	AGA	CTC	ACA	AAC	CTT	TAT	TTG	ACA	CGT
2070	2080	2090													
*	*	*													
ATC	CCC	TCA	AAA	AAA	AAA	CGG	AGA	TCC							
TAG	GGG	AGT	TTT	TTT	TTT	GCC	TCT	AGG							

Figure 4

Multiple Tissue Northern  
*bcl-2* and *cdn-1* hybridization

Random primed, Klenow-labeled fragments of *bcl-2* and *cdn-1* clones were hybridized to a multiple human tissue Northern blot (Clontech 7760-1), at a final concentration of  $1 \times 10^6$  cpm/ml for each probe. Blot was washed at high stringency.



Figure 5

cdn-2 gene sequence

```

      10      20      30      40      50      60
      *      *      *      *      *      *
TTT TAA TAT AAA TTA ATG TGC TCT ATT TAT AGA GAC AAT ACA TGA AAT ATA CTT AAT AAA
AAA ATT ATA TTT AAT TAC ACG AGA TAA ATA TCT CTG TTA TGT ACT TTA TAT GAA TTA TTT

      70      80      90      100     110     120
      *      *      *      *      *      *
AAT TCA AAT GTT ATA GAA CTG AAA AAG ATG AAA AGT AAA AAC AAC CTA TTC CCC AGA GGT
TTA AGT TTA CAA TAT CTT GAC TTT TTC TAC TTT TCA TTT TTG TTG GAT AAG GGG TCT CCA

      130     140     150     160     170     180
      *      *      *      *      *      *
AGC CAC TGT CCA TAG TTT CTA TTT TAG ATT CTT TCC TTT ATA CAA GAT TAT TAT AGC TTC
TCG GTG ACA GGT ATC AAA GAT AAA ATC TAA GAA AGG AAA TAT GTT CTA ATA ATA TCG AAG

      190     200     210     220     230     240
      *      *      *      *      *      *
TAT TTT TTG GTG TAT GAA CTG TAG TCC TAG AGG ATT TTA TTA GTT ATG AGT TCT ATA ACT
ATA AAA AAC CAC ATA CTT GAC ATC AGG ATC TCC TAA AAT AAT CAA TAC TCA AGA TAT TGA

      250     260     270     280     290     300
      *      *      *      *      *      *
AAG ATC CAT CAT CTT AGT TGC TAA GAA CGT AGA TAC TGA GAA CAT CAT TTA AAA AAA CAT
TTC TAG GTA GTA GAA TCA ACG ATT CTT GCA TCT ATG ACT CTT GTA GTA AAT TTT TTT GTA

      310     320     330     340     350     360
      *      *      *      *      *      *
TTT TGG CTG GCA CCT CAT GAT CAC TGG AGT CTC GCG GGT CCC TCA GGC TGC ACA GGG ACA
AAA ACC GAC CGT GGA GTA CTA GTG ACC TCA GAG CGC CCA GGG AGT CCG ACG TGT CCC TGT

      370     380     390     400     410     420
      *      *      *      *      *      *
AGT AAA GGC TAC ATC CAG ATG CTG GGA ATG CAC TGA CGC CCA TTC CTG GAA ACT GGG CTC
TCA TTT CCG ATG TAG GTC TAC GAC CCT TAC GTG ACT GCG GGT AAG GAC CTT TGA CCC GAG

      430     440     450     460     470     480
      *      *      *      *      *      *
CCA CTC AGC CCC TGG GAG CAG CAG CCG CCA GCC CCT CGG GAC CTC CAT CTC CAC CCT GCT
GGT GAG TCG GGG ACC CTC GTC GTC GGC GGT CGG GGA GCC CTG GAG GTA GAG GTG GGA CGA

      490     500     510     520     530     540
      *      *      *      *      *      *
GAG CCA CCC GGG TTG GGC CAG GAT CCC GGC AGG CTG ATC CCG TCC TCC ACT GAG ACC TGA
CTC GGT GGG CCC AAC CCG GTC CTA GGG CCG TCC GAC TAG GGC AGG AGG TGA CTC TGG ACT

      550     560     570     580     590     600
      *      *      *      *      *      *
AAA ATG GCT TCG GGG CAA GGC CCA GGT CCT CCC AGG CAG GAG TGC GGA GAG CCT GCC CTG
TTT TAC CGA AGC CCC GTT CCG GGT CCA GGA GGG TCC GTC CTC ACG CCT CTC GGA CGG GAC
      M   A   S   G   Q   G   P   G   P   P   R   Q   E   C   G   E   P   A   L>

      610     620     630     640     650     660
      *      *      *      *      *      *
CCC TCT GCT TCT GAG GAG CAG GTA GCC CAG GAC ACA GAG GAG GTT TTC CGC AGC TAC GTT
GGG AGA CGA AGA CTC CTC GTC CAT CGG GTC CTG TGT CTC CTC CAA AAG GCG TCG ATG CAA
      P   S   A   S   E   E   Q   V   A   Q   D   T   E   E   V   F   R   S   Y   V>

      670     680     690     700     710     720
      *      *      *      *      *      *
TTT TAC CAC CAT CAG CAG GAA CAG GAG GCT GAA GGG GCG GCT GCC CCT GCC GAC CCA GAG
AAA ATG GTG GTA GTC GTC CTT GTC CTC CGA CTT CCC CGC CGA CGG GGA CGG CTG GGT CTC
      F   Y   H   H   Q   Q   E   Q   E   A   E   G   A   A   A   P   A   D   P   E>

```

Figure 5 cont.

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                                >NcoI
      730          740          750          760          770          780
      *          *          *          *          *          *
ATG GTC ACC TTA CCT CTG CAA CCT AGC AGC ACC ATG GGG CAG GTG GGA CGG CAG CTC GCC
TAC CAG TGG AAT GGA GAC GTT GGA TCG TCG TGG TAC CCC GTC CAC CCT GCC GTC GAG CGG
M   V   T   L   P   L   Q   P   S   S   T   M   G   Q   V   G   R   Q   L   A>

      790          800          810          820          830          840
      *          *          *          *          *          *
ATC ATT GGG GAC GAC ATC AAC CGA CGC TAT GAC TCA GAG TTC CAG ACC ATG TTG CAG CAC
TAG TAA CCC CTG CTG TAG TTG GCT GCG ATA CTG AGT CTC AAG GTC TGG TAC AAC GTC GTG
I   I   G   D   D   I   N   R   R   Y   D   S   E   F   Q   T   M   L   Q   H>

>PstI
      850          860          870          880          890          900
      *          *          *          *          *          *
CTG CAG CCC ACG GCA GAG AAT GCC TAT GAG TAC TTC ACC AAG ATT GCC TCC AGC CTG TTT
GAC GTC GGG TGC CGT CTC TTA CGG ATA CTC ATG AAG TGG TTC TAA CGG AGG TCG GAC AAA
L   Q   P   T   A   E   N   A   Y   E   Y   F   T   K   I   A   S   S   L   F>

      910          920          930          940          950          960
      *          *          *          *          *          *
GAG AGT GGC ATC AAT TGG GGC CGT GTG GTG GCT CTT CTG GGC TTC AGC TAC CGT CTG GCC
CTC TCA CCG TAG TTA ACC CCG GCA CAC CAC CGA GAA GAC CCG AAG TCG ATG GCA GAC CGG
E   S   G   I   N   W   G   R   V   V   A   L   L   G   F   S   Y   R   L   A>

      970          980          990          1000          1010          1020
      *          *          *          *          *          *
CTA CAC ATC TAC CAG CGT GGC CTG ACT GGC TTC CTG GGC CAG GTG ACC CGC TTT GTG GTG
GAT GTG TAG ATG GTC GCA CCG GAC TGA CCG AAG GAC CCG GTC CAC TGG GCG AAA CAC CAC
L   H   I   Y   Q   R   G   L   T   G   F   L   G   Q   V   T   R   F   V   V>

      1030          1040          1050          1060          1070          1080
      *          *          *          *          *          *
GAC TTC ATG CTG CAT CAC TGC ATT GCC CGG TGG ATT GCA CAG AGG GGT GGC TGG GTG GCA
CTG AAG TAC GAC GTA GTG ACG TAA CGG GCC ACC TAA CGT GTC TCC CCA CCG ACC CAC CGT
D   F   M   L   H   H   C   I   A   R   W   I   A   Q   R   G   G   W   V   A>

      1090          1100          1110          1120          1130          1140
      *          *          *          *          *          *
GCC CTG AAC TTG GGC AAT GGT CCC ATC CTG AAC GTG CTG GTG GTT CTG GGT GTG GTT CTG
CGG GAC TTG AAC CCG TTA CCA GGG TAG GAC TTG CAC GAC CAC CAA GAC CCA CAC CAA GAC
A   L   N   L   G   N   G   P   I   L   N   V   L   V   V   L   G   V   V   L>

      1150          1160          1170          1180          1190          1200
      *          *          *          *          *          *
TTG GGC CAG TTT GTG GTA CGA AGA TTC TTC AAA TCA TGA CTC CCA AGG GTG CCT TTG GGG
AAC CCG GTC AAA CAC CAT GCT TCT AAG AAG TTT AGT ACT GAG GGT TCC CAC GGA AAC CCC
L   G   Q   F   V   V   R   R   F   F   K   S   *>

      1210          1220          1230          1240          1250          1260
      *          *          *          *          *          *
TCC CAG TTC AGA CCC CTG CCT GGA CTT AAG CGA AGT CTT TGC CTT CTC TGC TCC TTG CAG
AGG GTC AAG TCT GGG GAC GGA CCT GAA TTC GCT TCA GAA ACG GAA GAG ACG AGG AAC GTC

                                >Hind3
      1270          1280
      *          *
GGT CCC CCC TCA AGA GTA CAG AAG CTT
CCA GGG GGG AGT TCT CAT GTC TTC GAA

```

Figure 6 Amino acid sequences of cdn-1, cdn-2, and bcl-2 family proteins

cdn1	masgggpppprqqcgepalpsaaseeqvaqdtteevfrrsyvfyrrhqgeaeagvaapadpemt	
cdn2	masgggpppprqqcgepalpsaaseeqvaqdtteevfrrsyvfyrrhqgeaeagvaapadpemt	
bcl2	mahagrtgyDNREIVMKYIHYKLSQRYEWdagvgaappgaapqifssqpghtphtaaardpvarspiqtpaapga	
bax	mdgsgeqprgggptseeqimktgalllqgfiqdragrmggaep	
bcl-x	msqSNRELVDFLSYKLSQKGSWSqfsdveenrteaegtesemetpsaingnpswhladsavngatghsssl	
mcl-1	...(+123 aa)eldgyepeplgkrpavlpillelvgesGnntstdgslpstppaeeedelyrqaieiisrylreगतakdtk	
A1	maeselmhihsaehylgyvlq	
bhbf	maystreillalcirdervhngntlhpvlelaar	
LMW5-HL	megeeliyhniineilvgv	
ced9	mtrctadnsltnpayrrrtmatgemkeflgikgteptdfginsdaqdlpspsrqastrmsigesidgkindweeprldIEGFVVVDYFTHRIRQNGMEWfgapg	
cdn1	lplqpsstmgQVGRQLAIIIGDDINRRYDSEFQTMLOHLOPTAENAYEYFTKIATSLFESGI-NWGRVVALLGFGYRLALHVVYQHGLTGFLGQVTRFVVDFMLHH	
cdn2	lplqpsstmgQVGRQLAIIIGDDINRRYDSEFQTMLOHLOPTAENAYEYFTKIATSLFESGI-NWGRVVALLGFGYRLALHVVYQHGLTGFLGQVTRFVVDFMLHH	
bcl2	agpalspvpvVHLTLRQAGDDFRRYRRDFAEMSRQLHLtpfargFATVVEELFRDGV-NWGRIVAFEFEGVMCVESVNRMSPLVDNIALWMTEY-LNR	
bax	elaldpvpqdaastkklsecikrigdeldsnmelgrmiaavtdsprevFFRVAADMFSDGNFNWGRVVALFYFASKLVKLKALCTKVPDELIRTIMGWTLDL-LRE	
bcl-x	darevipma-AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFQVVMELFRDGV-NWGRIVAFEFEGVMCVESVNRMSPLVDNIALWMTEY-LNR	
mcl-1	pmgrsgatsrkaLETTLRRVGDGVQRNHEFVTFQMLRKLDIKNEDDVKSLSRVMIHVFSDDGVNWRGRIVTLISFGAFVAKHLKTINQESCIPLAESITD-VLVR	
A1	vpafesapsqacrvlgrvafsvqkeveknksyllddfhvesidtarliFNQVMEKEFEDGIINWGRIVTIFAFGGVLLKKLPqeialdvcaykqvsfvaefi	
bhbf	etplrlspedtvvlryhvlleelernsetfttetwnrfithtehvdldfnsvfleifhd-LINWGRICGFIVFSARMAKYCKDANN-HLESTVITTAYNF-SEG	
LMW5-HL	ikyyymndihelspyqqikliltydeclnkqvtitfsltnaqeiklQFTGVVTELFKrgdpslgralamawcmhacrtlccnqstpyyvvvdlsvrgmleam-	
ced9	lpcgvqpehemmrvmgtifeekkhaenfetfceqLlavprisfslgydvrvrtvgnagtdqcpMSYGRLLIGLISFGGFVAAKmesvelqgqvrvnlfvytslfiKT	
cdn1	CIAR--WIA-QR-GGWVAALNLGngpilnvlvlgvllgqfvvrrffks	SEQUENCE IDENTITY:
cdn2	CIAR--WIA-QR-GGWVAALNLGngpilnvlvlgvllgqfvvrrffks	cdn1/cdn2 = 97%
bcl2	HLHT--WI--QDNGGWDFAVELYgpsmrplfdfswlslktllslalvgacitlgaylghk	
bax	RLLG--WI--QDQGGWDGLLSYfgtptqvtifvagvltasltiwwkmg	
bcl-x	HLEP--WI--QENGWDTFVELYgnnaaaesrkqgerfnrwlftgntvagvllgslfsrk	
mcl-1	TKRD--WLVKQ--RGWDGFVEFFhvedleggirvnllafagvagvagalylir	
A1	MNNTGEWI-RQ-NGWEDedgfiikkfepksgwltflqmtgqiwmflfk	
bhbf	-LDG--WIHQQ--GGWStliedniipgsrrfswtflagltlllvcisyflfisirgrh	
LMW5-HL	KHNLPPWMISH--GGQEEFLAFslhsqiyvifnikyflskfnhhfrscvqlirkcnli	
ced9	-RIRNNWKE-H-NRSWDDFMTLgkqmkedyeraaeakvgvrrkqnrrwsmigagvtagagivgvvvvcgrmmfslk	

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 120  
 ATAAATTGTA AACTTCTGGT AATAATCTAC GACTCTACAA GAGGCAATAG GGTACTGTGT ACAGAGAGCA GGTCTTGTAA  
 180  
 ACACACAGA CTGGTTTAG ATCTCTGAC TCAACCACT GTGTGACTTG CCAAGCTTC TCACTCTCT TAAAGGCCA  
 240  
 TCTGTGTATC TGTACAGGAA TGAATGAAAG AGTATGTGCA CCAAGCTAT CCAAGCTCA GGTAAATTA TTGCTTGGG  
 300  
 TTTTAACTA AATTGTTCAA GCTCATGACA TTCTAGGAGA AAAGGCTAG TGTCTCTTC TTAAGGTGAT TGTGTGATG  
 360  
 TGTCTTCCAG GAATCTATG GCTTCTCAA CCAATCTA CCGTGGCTT GACCAATGG CTGACCACT TCACTGATC  
 420  
 TGTCTGATG ACACAGCTG CACTCAGCA CTGCGCTGC AGGTAGAAG GATTTCTAG TGGCATTA CTTGGGATA  
 480  
 CCACATGGG ACCATGTCA CAGATTTCT GTTACAGTCC ACCCGGACC ATTCTTCTC AATCATAA CTCTTACAG  
 540  
 GAGAGCTAGG TCAAGCACC ATGACATAA CACCAAGCT TCGTACAA CTCAAGCTCT ATCTTATG TCAAGCAAT  
 600  
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 660  
 CCTCTTCTC AGGTCTGAC ACTGAAAGT AAGACAGCT TCTTATGCT ATATTTCAA AATTTGCTT ATACCTTCT  
 720  
 CTCAGGACAA CAGTGGCTG CTTAAGAGCC TTATCTTGT GTACTGTA TTTTCTTC CCGTACCTT CCAAGGCTA  
 780  
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 840  
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 900  
 TAAAGCTGA CAGTGGCTC CATTGCAAT AGAGGACAC TCAGACAAA CTTTGGCTT CTTGTGGA GACTGACCA  
 960  
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 1020  
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 1080  
 AGTTTCTCA TGTATCTT TTCTGCTGCT TGTGTGAT ATTTGCTTA CATTGCTTA AATATATTA AATACATTA  
 1140  
 ATCACTGAG TCTCAGGCT CCGTGGGCT ACACAGGAC AGTCAAGCT CACATGAGA TACCAAGAT CACTGACCT  
 1200  
 CCGTCTCTG AAGCTGGCT CCACTCACT CCGTGGGCT AOCAGCTCT AGCGCTCTG GACTCTCACT TCAAGCTCT

TGACGCAAGG GGGTTCAGC AGCATGCTG GAGGCTGCA CTGTCTGCA CTGAGAGCTG AAAA ATG GCA TGG GGG  
M A S G>

1680

CXA GGC CCA GCG GCT GCG AGG CAG GAG TGC GGA AAG CTT GGC CTG GCG TCT GGT TCT GAG GAG CAG  
Q G P G P P R D B C O K F A L P S A S K E Q>

1760

GTA GGC CAG GAC ATG GAG GGG TTT TCC GCA GCT AGG TTT TTT ACC ACC ATT AGC AGC AAC AGG AGG  
Y A Q D M K G P S A A T P P T T I S R N R R>

1840

CTG AAG GGG GGG GCG GCG GCG ACC CAG AGA TGG TCA GCT TGC GCG TCC AAC CTA GCA GCA GCA  
L K G R P P L P T Q R M S P C P S K L A A P>

1920

TGG GCG AGG TGC GAC GCG AGG TCG CCA TCA GCA GGA CCA CAT CAA CTG GCA CTA TCA CTTCGGAGT  
M G R M D G S S P S P G R K Q P A L >

2000

TCCGAGCAT GCTGAGCAG CTGAGGCTA GCGAGAGAA GCGTACGAG TACTTACCA AGATGCGCTC GAGCTCTCTT

2080

GAGAGTGCA TCAACGGGG GGGTGTGCTG GTCTCTCTG GCTTCGGCTA GCGTCTGCTC CTACATCTCT ACCAGCACCG

2160

CTTGACTGCG TTCTGCGCC TGGTGAACCG CTGCGTCTG TCAATGCTG AACAAGCAT TCGCGGTG ATCTGACAGA

2240

GCGGCGCTG GGTGCGGCG CTGCACTTGG GCAATAGTGC CATGCTAAC GGTGCTGCG TTGTGGGTGT GTTCTCTCTG

2320

GCGCAATTG TGGTAAAGG ATCTCTCAA TCACTACTGC CAGGGTGTG CTTCGGGTC CCACTGTGA GCGTCTCTG

2400

GACTTAAGCC AAGTCTTTG CTTCGCACT GCGTGTGAG GGTCAAGCTT CAAAGTACA GAAAGCTGAG CAAGTGTGCA

2480

GCGGCGCTG GAGGGGCGG TGGTGGGGG CCACTGAGG TCGGAGGCA CCTCAACAT GCAAGTGTG ACTGGGCGCT

2560

CTCTCTGCG CCAGGGCTG TCGGCTCTG CTTGCACTT CTGGAAGCTC CTATCTTTC TCTGCTAGG GCTGAGAGG

2640

CTGATTAATY GGGGAAGCA GAGCTGGA GCACTCTCTC CCAAGTAACT GTTAAAGGT TTAGCTTTT TAAATATCC

2720

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2800

GCAAGATTC AGCTATCTG GAGATCAGA GCTAAGAGC TAGGACTGA TCTGCTCTT GCGCTGCTT AAGCATCATG

2880

TGTCCAGGA GCAAGACTA CTGGAGAGG GACCAAGGT CTTACCAAG TCTGCGCTG GCGCAATTC TGTCTGCGC

2960

ATACTGCTT TCAAGTGA CTCTCAAGG TCTGCGCTT GCGGTGCGG GCGGGTGA GTAAGAGGC AAGCTCTCT

3040

GACTTATGT GTCAGAGGC TCAAGGCTG GTCGCAAGG TGTCTTACG TCTCTGCTT GCTCTCTCT TATCATACT

3120

TGTCTTAC CATTCACTA CAGGTGAAG GCTTCAAGG TGTCTGCGG CTTGTGTA GGTATGCGT AAGGCTCTC

1200  
CCGCCGAGA CTACAGGCT TGGTTAGGG CTGGTTTGT TATTTCAGG ATAAAGATA GCGACTTCAT CTGGAGGTT  
1280  
CTAAGTGGG CAGAGACTAT CAACAGCACA GGAATCCAG AGGTGGATC CTCCCTCATG GCTCTGGCAG AGTGTAAATCC  
1360  
AGGGTGGAG ATAGCGAAT GTGAATAGCT GAATCTGTC GGGGAGGCT CCAAGCTCTT CACCTTTCTG GCTCTCTGCT  
1440  
CAATGTTGG GTGAGGTAC CTCTCTATC GGGCAGACC TAGGCTGTTT GGGGTGAAG GGGAGAACTT CTGATTCAG  
1520  
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1600  
CCATTAATAA AAAAAGGAG AAAAAATGT AAAAATCAT CTTAGCTTAA AGCTACTTAT AGGGGATAA AGCAGGACT  
1680  
GTATATGAG ACAAAATAC ACTTAGAGG AAGAAATAG TTCTGTGAG CACGCTGTC TCACAGCTCT AACTCCAGCA  
1760  
CTTGGGAGA CCAAGTGGG AGATCTTTT GATTCAGGA GTTGGAGAC AGCTTGACA ACATAGCAAG ATCTTATCTC  
1840  
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1920  
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2000  
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2080  
TTGTGATTT CAAATAGCT ACAAGAGAG ATATGAAGT TTGCTGAAA CAGGAAATGA TAACTTGA GGTGACAGT  
2160  
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2240  
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2400  
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2480  
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2560  
GGCTGCAAC ATCAGAGAT ATCCCTGAT GGAAGCTGA GTTAAATTA GCTGAGGCT TGGGCTTC CAGGCTGTT  
2640  
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2720  
GCTCTGTAT TATTACTGA GTTCTGAG GGGCTGAT TGTCTCTGT CCAAGAAAT AACTACATG TTATAGAAA  
2800  
TATTGAGG GGGGCTGCT GCTTCAAGC TGTATGAG CACTTTGGA GGGCAAGCA GCTGATCAT GAGGTGAGA

## Figure 7 cont.

4880  
GTTTCAGACC ATCATGCOCA ACATGCTGAA ACCOCHTCTC TACTTAAATC ACAAAATTA CCTGCTGTCTG CTGCGCGZCA

4960  
OCTGVAGTCC CAGCTACTCC CGAGCCTGAG CCAGGAAAT CCTTTCAGCC TCGGAGCCCG AGGTTCACCT GACCGATAT

5040  
CACGCCACTG CACTDCAGCC TCGGACAGA CCGAGACTCC ATCTCAAAA AAAGAAAAA TAAATACCTG AAATTAAGAC

5120  
TCCCATATA GACAAAAA AATTTATTA AGTAAAAA TAAATAAAA TACAGCTCC AGGTCTGATT GCGCCAGAG

5200  
GCTGTAGGAC ACAGACCCDC AGCAATGAC TTCATAAATC CCGTGTATTA TCAGCTCAC CTGCGAATTT GCGGACCGCA

5280  
CTCATTTTAA AACAGTTTCC TCGATTCTTA CCGAACCAG AAAATCAGAC TCTTTCAGCT AAATTCCTTA GCTCCCTGCT

5360  
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CTCTCTCTCT ATTCGCCAG GAGAAATC

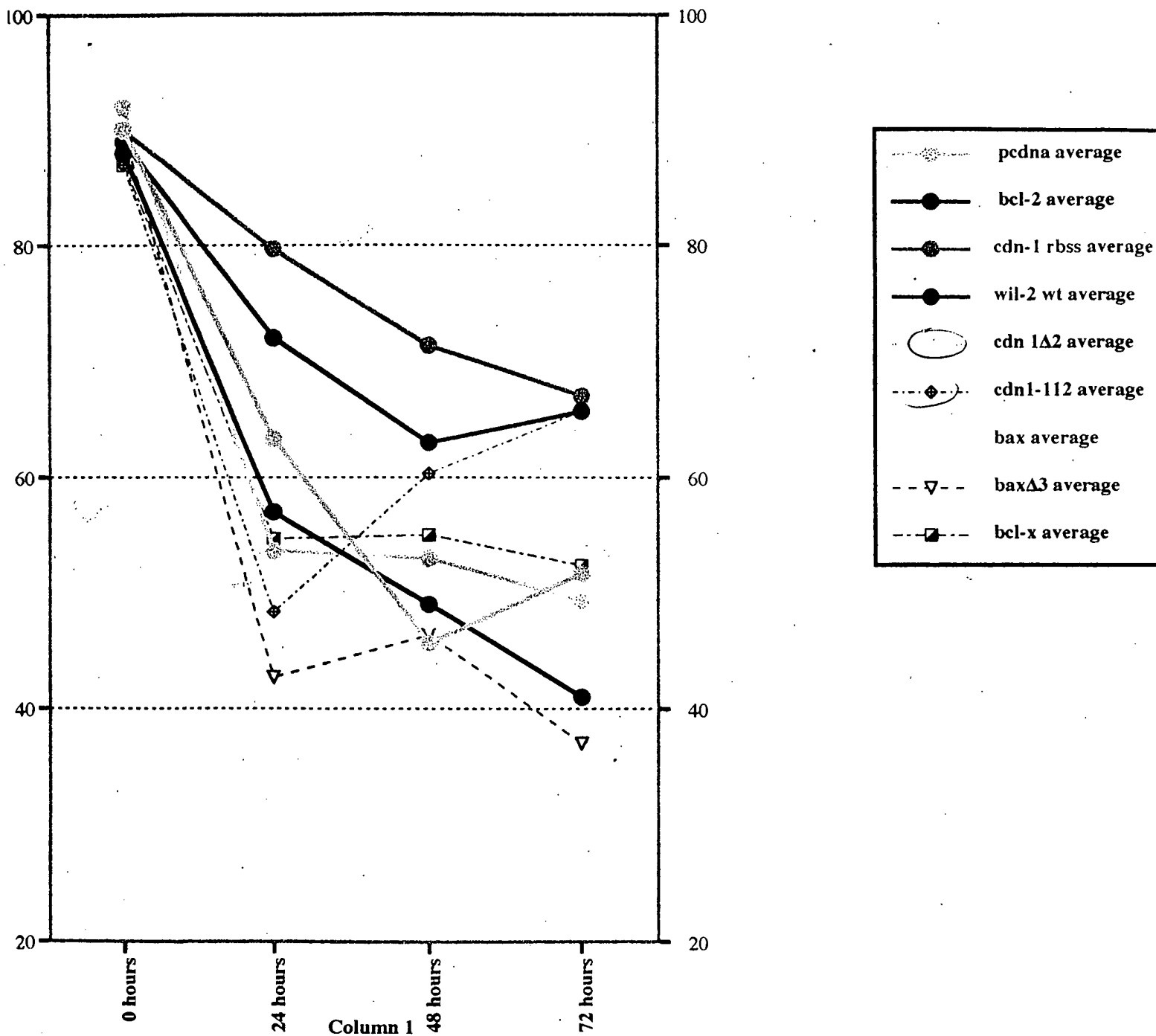




Figure 9

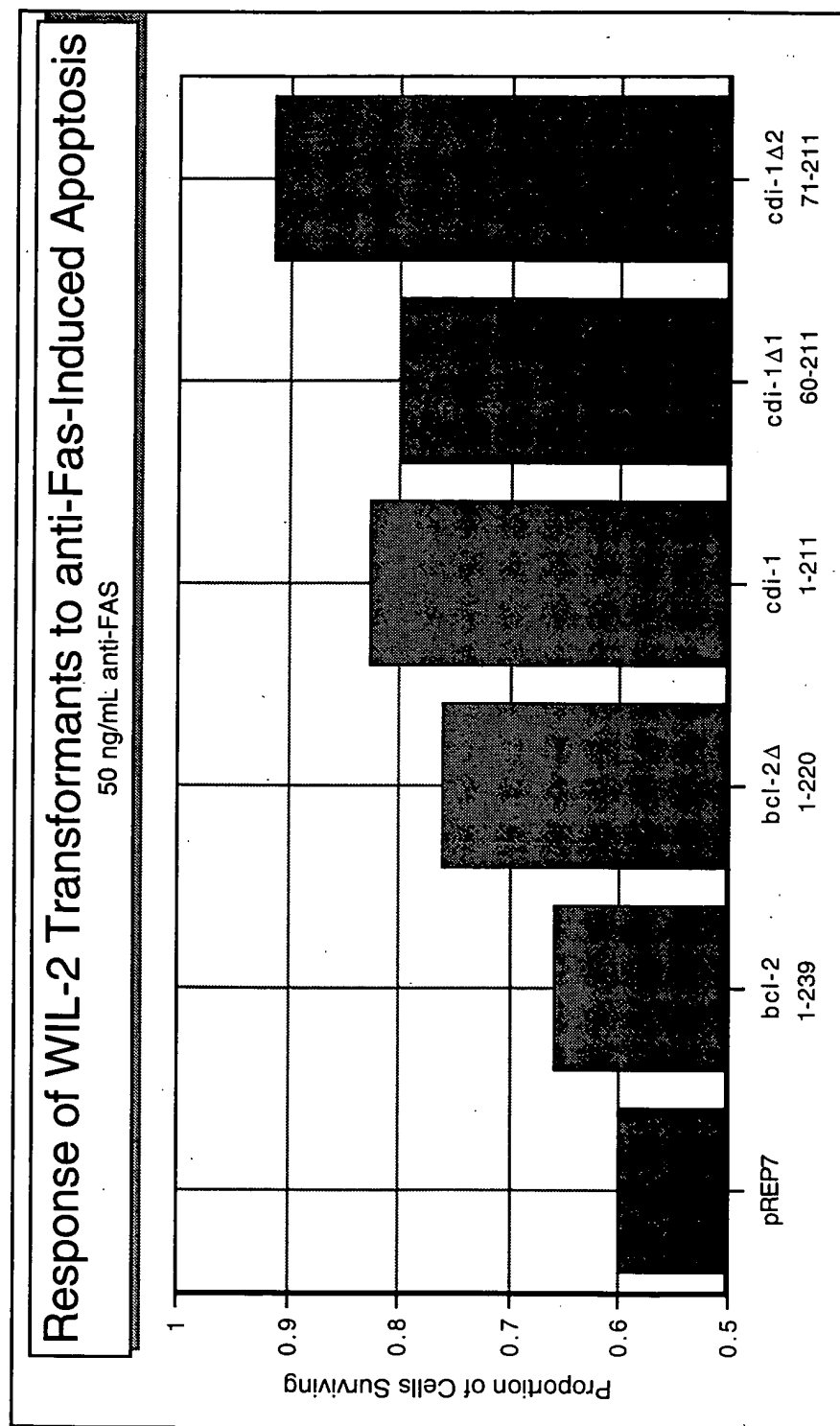


Figure 10

F15.12 transformants - IL-3

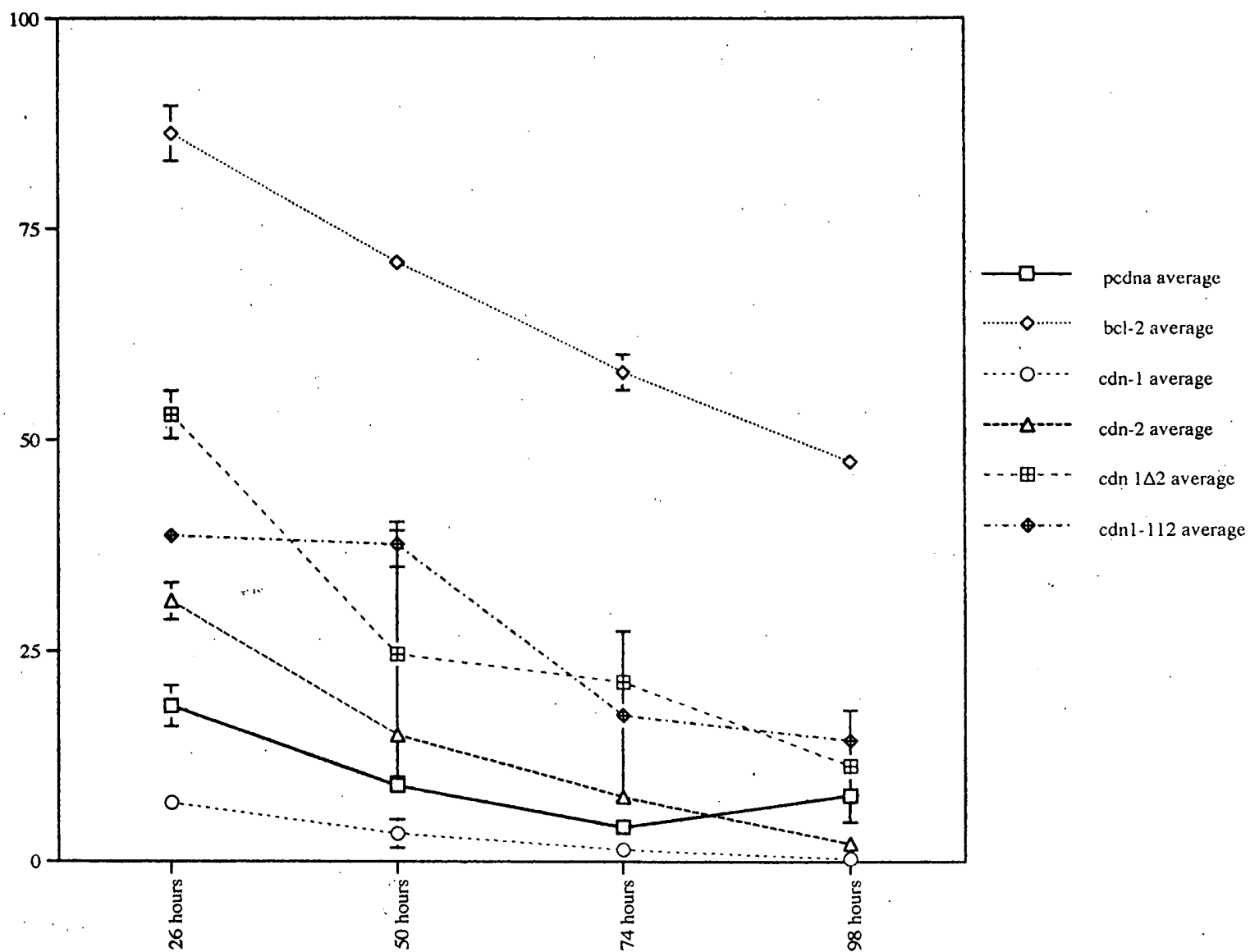


Figure 11 N-terminal methionine residues of cdn-1 derivatives

$\Delta 2$   $\Delta 3$   $\Delta 1$   
LPLQPSSTMGQVGRQLAIIIGDDINRRYDSEFQTMQLQHLQPTAENAYEYFTKIATSLFESGNWGRVVALLGFGYRLALHVYQHGLTGFLGQVTRFVVDFMLHH  
CIARWIAQRRGGWVAALNLGNLGNLNLVVLGVLLGQFVVRFFKS  
MASGQGPGRPRQECGEPALPSASEEQVAQDTEEVFRSYVFYRHQQEQEAEGVAAAPADPEMVT